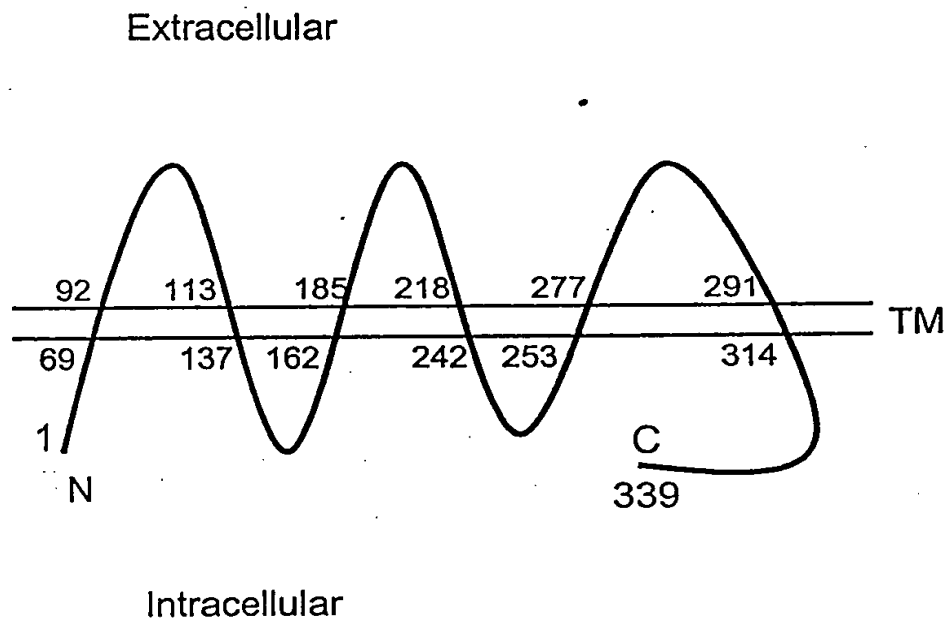


**FIG. 1A**

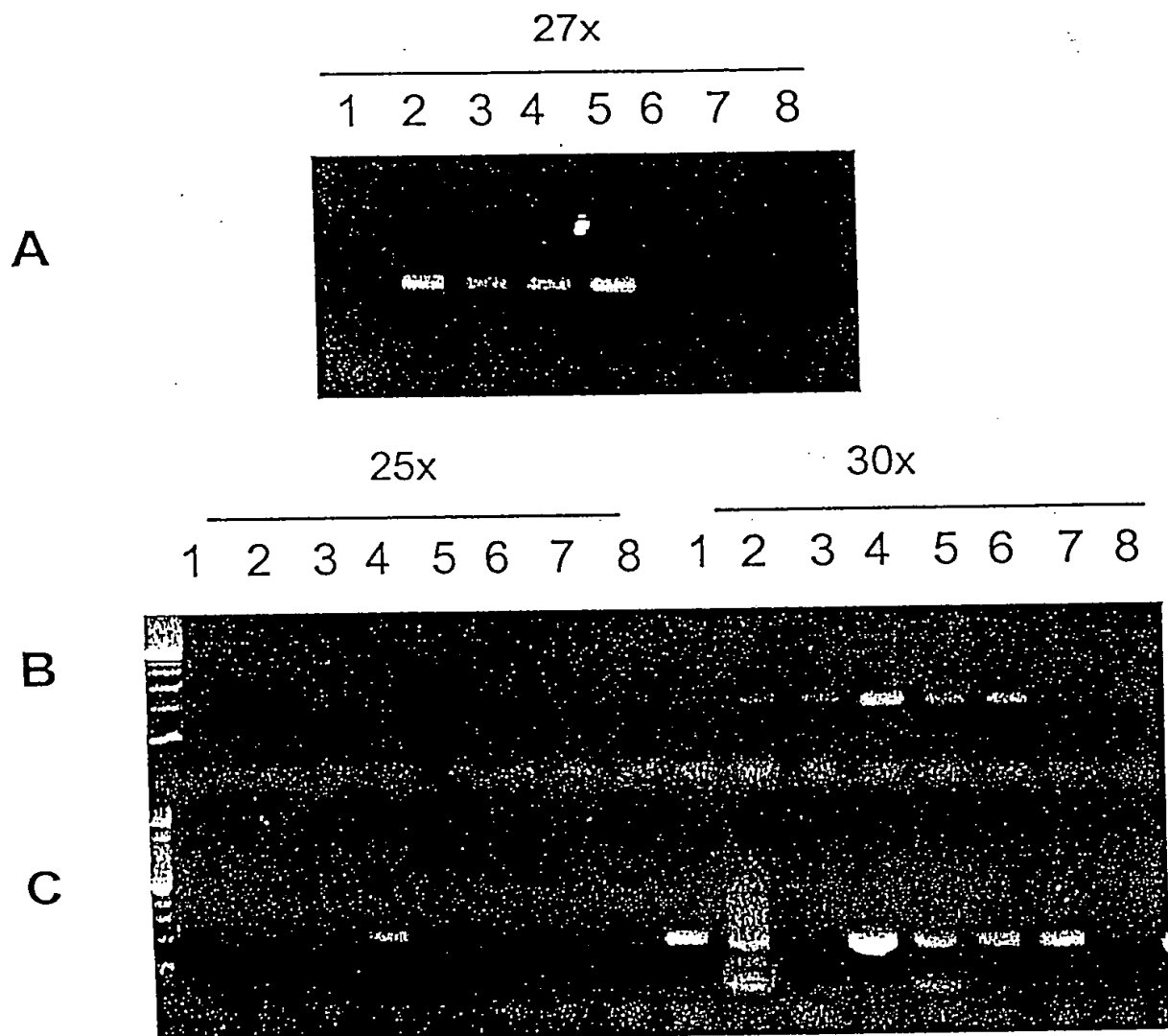
FIG. 1B



## FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG  
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT  
AAC AGC AAG 3' (SEQ ID NO:3)

FIG. 2



## Panels:

## A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

## B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

## C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

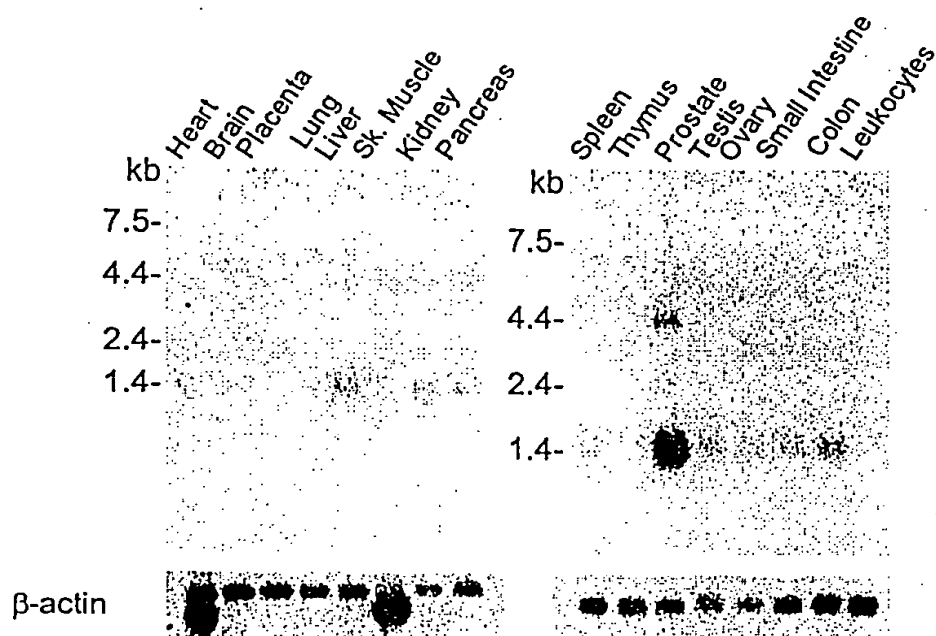


FIG. 3B

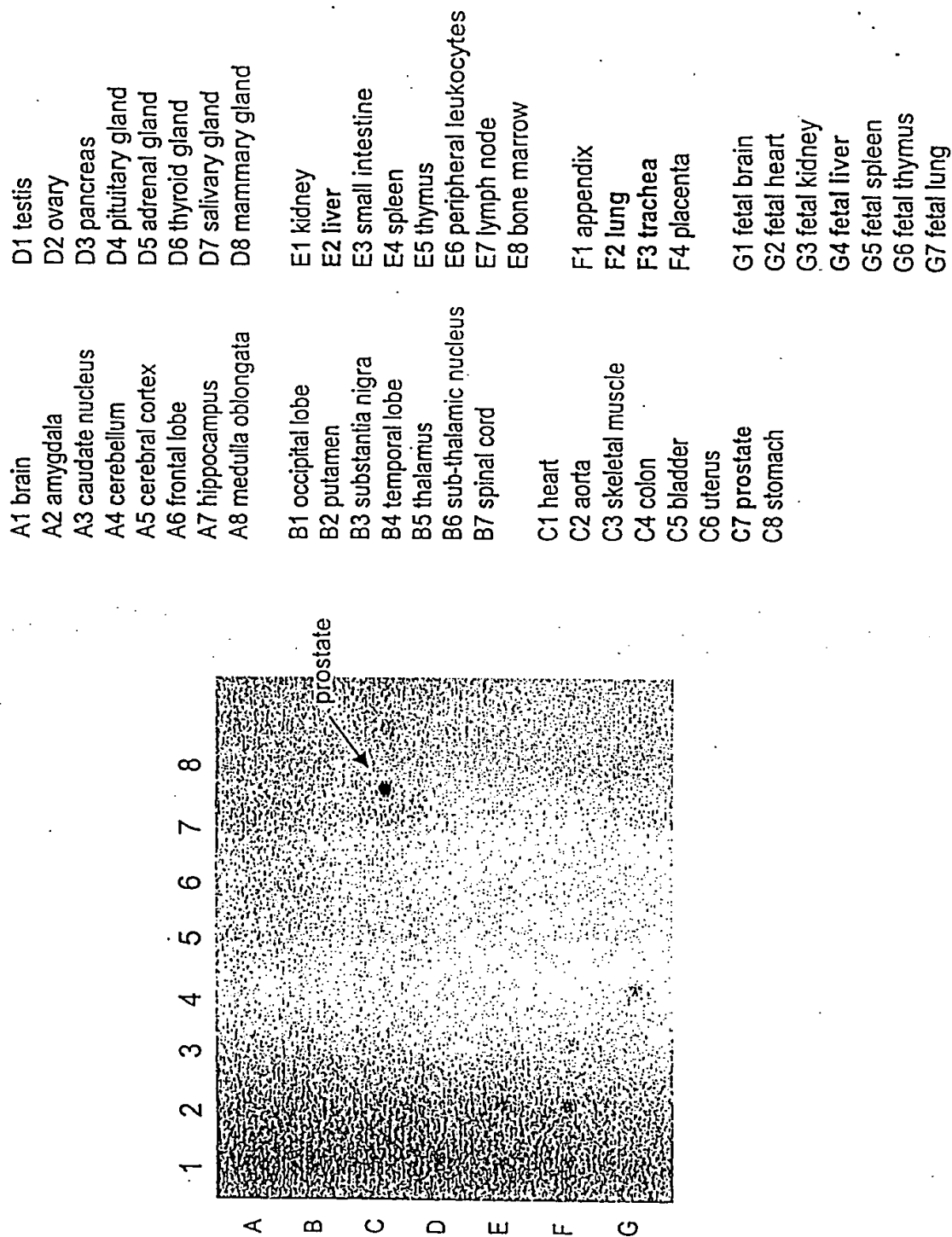


FIG. 4-1

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC  
ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG  
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC  
ATTTGCACCAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA  
GTGGCACTTGCCAATTAATAAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT  
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG  
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTCATAATGGAACCAA  
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT  
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT  
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT  
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG  
AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT  
ATAGAATATGTTGACTTTACCCCATAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT  
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAGGCAT  
TAAATATTCTTTGTTTTTTTTTTTTGTTTGTGTTTTTTTTGTTTGTGTTTTTTGAGATGAAGTCTCG  
CTCTGTTGCCATGCTGGAGTACAGTGGCAGCATCTCGGCTCACTGCAACCTGCGCTCCTGGGTTCAGGCGATT  
TCTTGCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTA  
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCTCCC  
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTCTAATATTTGAAACTTGTTAGACAATTT  
GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTAAAAAAATATTCTTTTACC  
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAACTCTCTCCTTGAAA  
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT  
ACTTACTCACTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT  
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA

FIG. 4-2

TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT  
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC  
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTAATTTTGTAGGTTTCTAG  
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA  
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA  
ATACCTAGCCATAATAGGTATACAATACACATTTGGTAAACTAATTTTCAACCAATGACATGTATTTTCAACT  
AGTAACCTAGAAATGTTTCACTTAAATCTGGAAGTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA  
ACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT  
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTGAGAACACCGT  
TGAGATTACATAGGTGAACAACTATTTTAAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA  
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC  
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTATTATTATTTATCAAAATCAGAGTGAATCA  
CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT  
TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT  
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAATAAATATCATAAG  
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG  
TTCACCTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG  
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG  
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTCCTTTTGCAGAGCAAGCTAGGA  
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG  
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGCTCTGATATTTAAAGCATACTATT  
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG  
ATATGTTCCAGTTGTAGAACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCACATTTCA  
AGTTTGTATTTGTTAATAAAATGATTATTCAGGAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:6)

FIG. 5

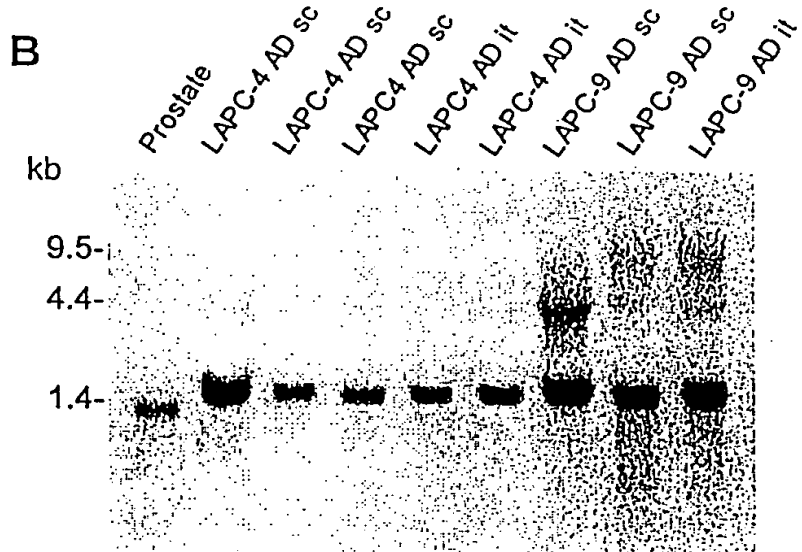
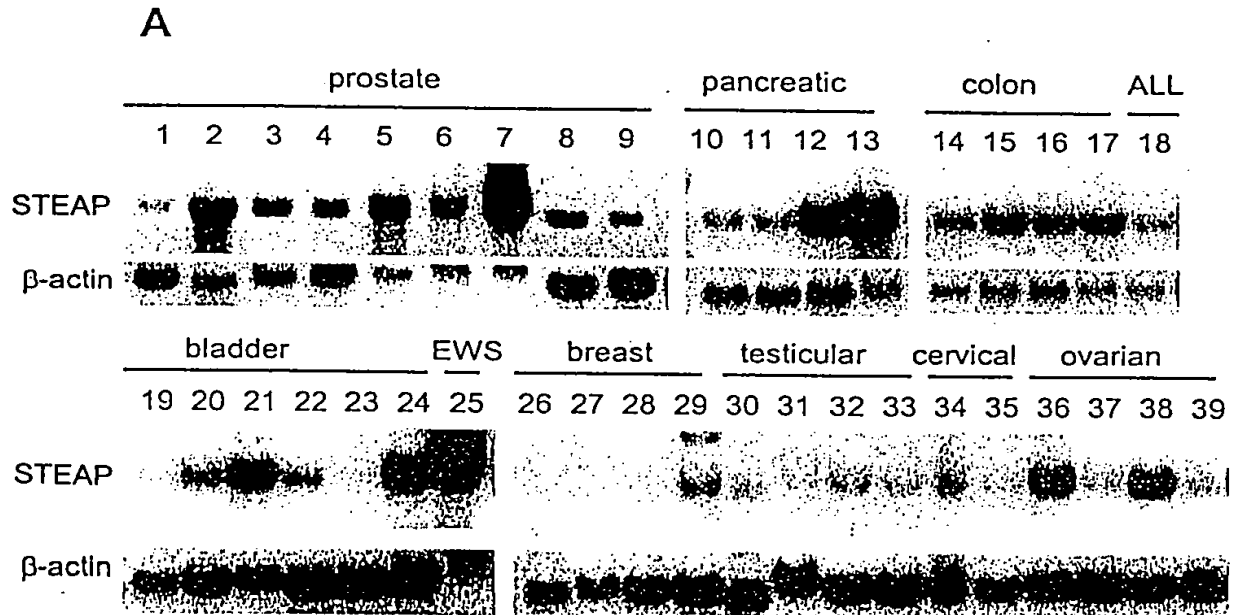
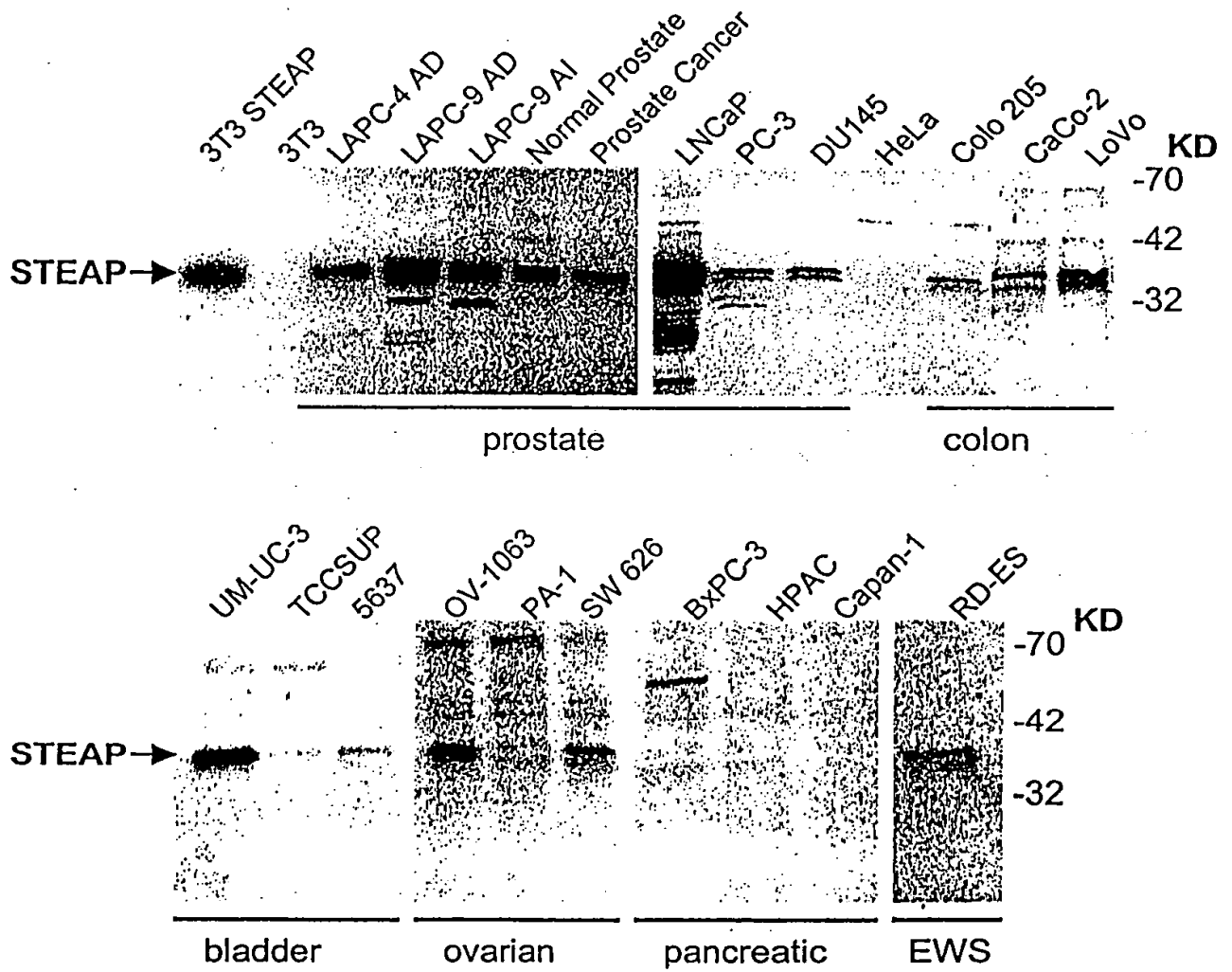
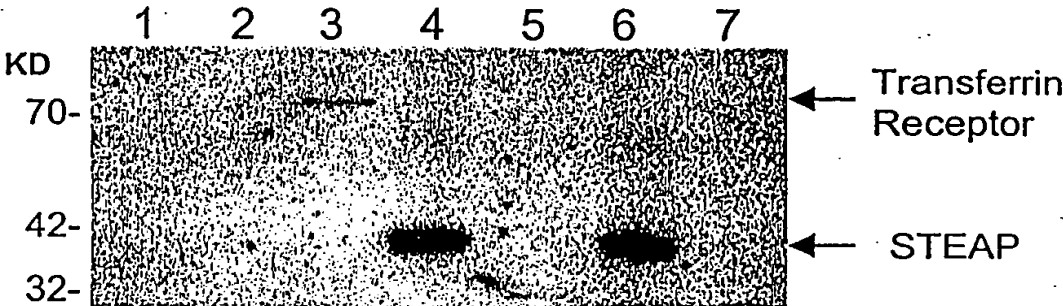


FIG. 6



**FIG. 7**

**A**



# B

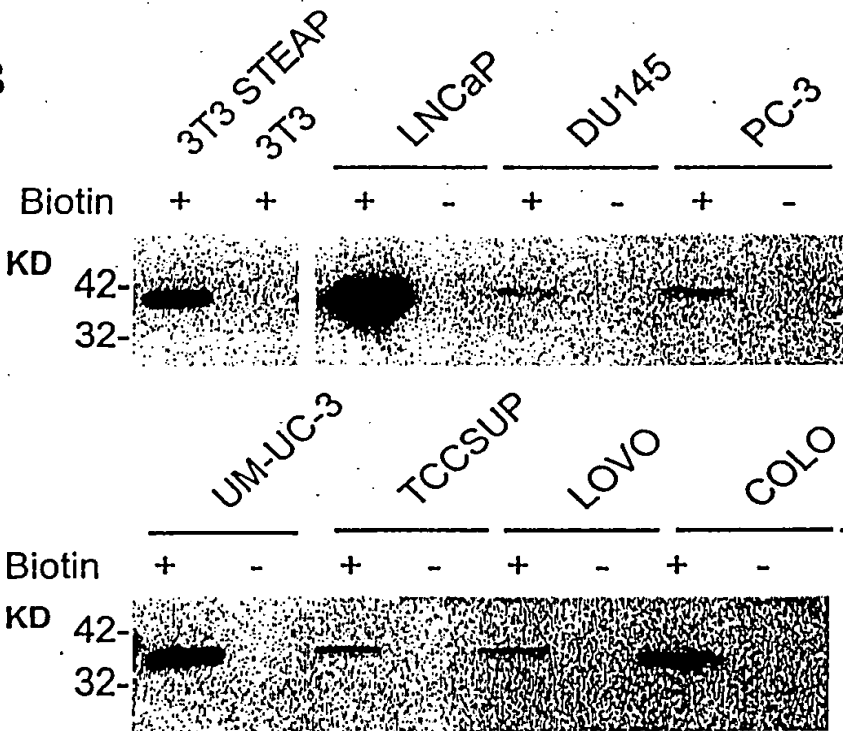


FIG. 9

		10		19		28		37		46		55						
5'	GAC	TTT	TAC	AAA	ATT	CCT	ATA	GAG	ATT	GTG	AAT	AAA	ACC	TTA	CCT	ATA	GTT	GCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Asp	Phe	Tyr	Lys	Ile	Pro	Ile	Glu	Ile	Val	Asn	Lys	Thr	Leu	Pro	Ile	Val	Ala
		64			73			82		91		100					109	
	ATT	ACT	TTG	CTC	TCC	CTA	GTA	TAC	CTC	GCA	GGT	CTT	CTG	GCA	GCT	GCT	TAT	CAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Thr	Leu	Leu	Ser	Leu	Val	Tyr	Leu	Ala	Gly	Leu	Leu	Ala	Ala	Ala	Tyr	Gln
		118			127			136		145		154					163	
	CTT	TAT	TAC	GGC	ACC	AAG	TAT	AGG	AGA	TTT	CCA	CCT	TGG	TTG	GAA	ACC	TGG	TTA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Tyr	Tyr	Gly	Thr	Lys	Tyr	Arg	Arg	Phe	Pro	Pro	Trp	Leu	Glu	Thr	Trp	Leu
		172			181			190		199		208					217	
	CAG	TGT	AGA	AAA	CAG	CTT	GGA	TTA	CTA	AGT	TTT	TTC	TTC	GCT	ATG	GTC	CAT	GTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Gln	Cys	Arg	Lys	Gln	Leu	Gly	Leu	Leu	Ser	Phe	Phe	Phe	Ala	Met	Val	His	Val
		226			235			244		253		262					271	
	GCC	TAC	AGC	CTC	TGC	TTA	CCG	ATG	AGA	AGG	TCA	GAG	AGA	TAT	TTG	TTT	CTC	AAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	Glu	Arg	Tyr	Leu	Phe	Leu	Asn
		280			289			298		307		316					325	
	ATG	GCT	TAT	CAG	CAG	GTT	CAT	GCA	AAT	ATT	GAA	AAC	TCT	TGG	AAT	GAG	GAA	GAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu
		334			343			352		361		370					379	
	GTT	TGG	AGA	ATT	GAA	ATG	TAT	ATC	TCC	TTT	GGC	ATA	ATG	AGC	CTT	GGC	TTA	CTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Val	Trp	Arg	Ile	Glu	Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu
		388			397			406		415		424					433	
	TCC	CTC	CTG	GCA	GTC	ACT	TCT	ATC	CCT	TCA	GTG	AGC	AAT	GCT	TTA	AAC	TGG	AGA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Leu	Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	Arg
		442			451			460		469		478					487	
	GAA	TTC	AGT	TTT	ATT	CAG	TCT	ACA	CTT	GGA	TAT	GTC	GCT	CTG	CTC	ATA	AGT	ACT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	Leu	Ile	Ser	Thr
		496			505			514										
	TTC	CAT	GTT	TTA	ATT	TAT	GGA	TGG	AAA	CGA	GCT	3'	(SEQ ID NO:7)					
	---	---	---	---	---	---	---	---	---	---	---	---						
	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	(SEQ ID NO:8)						

## FIG. 10

STEAP-2, AA508880 (NCI\_CGAP Pr6)

ggtcgacttttccctttattccctttgtcagagatctgattcatocatatgctagaaaccaacagagtgcactttttaca  
aaattccctatagagatttgtgaataaaaaccttacctatagttgccattactttgctctccctagtataaccttgcagg  
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttgggtggaaacctgggtta  
cagtgtagaaaacagcttggattactaagttgtttcttcgctatgggtccatgttgccctacagcctctgcttaccga  
tgagaagggtcagagagat (SEQ ID NO:9)

STEAP-2, 98P4B6 SSH fragment

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAAGTGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAGCG  
GCTGCCCATTACATTCCTCAGCTGTCTTGCAGTTAGGTGTACATGTGACTGAGTGTTGGCCAGTGAGATGAAGTC  
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT (SEQ ID NO:10)

AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcataatgtggctttgggaataacttgggtttt  
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcactggagagagttccgatttgt  
ccagtccaaactgggttatttgacctgatcttgtgtacagcccacacctgggtgtacgggtgggaagagattcctc  
agcccttcaaattctcagatgggtatcttccctgcagcctacgtgttagggcttatcattccttgcactgtgctgggtga  
tcaagtttgcctaatcatgccatgtgtagacaacaccttacaaggatccgccagggtgggaaaggaactcaaa  
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaaaa (SEQ ID NO:11)

R80991 (placental EST)

ggccgcggcancgcgtacgacctgggtcaacctggcagtcagcaggtcttggccanacaagagccacctctgggtg  
aaggaggaggtctggcggtggagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggccg  
tgacctcactgccgtccattgcaaaactcgctcaactggaggagttcagcttcgttcagtcctcactgggtcttgt  
ggccttcgtgctgagcacactncacacgctcacctacggctggacccgcgccttcgaggagagccgctacaagttc  
tacctncctcccaccttcacgntcacgctgctgggtgacctgcgttcgttcacctcgtggccaaagccctgttntac  
tgccctgcattcagccgnaga (SEQ ID NO:12)

## FIG. 11A

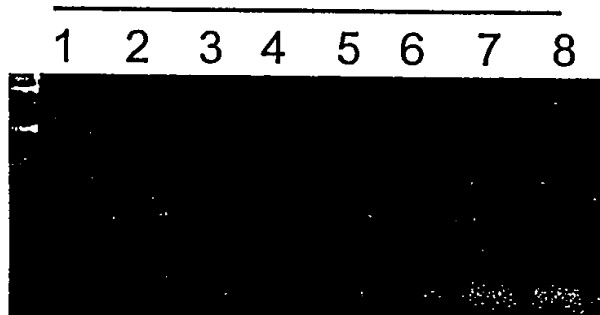
STEAP-1	106	FYKIPILVINKVLPMSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKMWLTRKQFG
STEAP-2	2	FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPWLETWLQCRKQLG
		***** ** * * * * * * * * * * * * * * * * * * *
STEAP-1	166	LLSFFFAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV
STEAP-2	62	LLSFFFMVHVAYSCLCPMRRSERYLFLNMAYQQVHANIEHSWNEEEVWRIEMYISFGIM
		***** * * * * * * * * * * * * * * * * * * *
		(Portion of SEQ ID NO:2)
STEAP-1	226	GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWN <sup>↓</sup> K
STEAP-2	122	SLGLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
		* * * * * * * * * * * * * * * * * * * * * * *
		(Portion of SEQ ID NO:8)

# FIG. 11B

	1	15	16	30	31	45	46	60	61	75	76	90
STEAP-1	MESRNDITNOEELKK	MKPRNLEEDDYLEK	DGETSMKGRFVLH	LHQTAAHAEFDCPSE	LQHTQELFPQWHLPI	KIAAIIASLTFLYTL						90
STEAP-2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	0
STEAP-3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	0
STEAP-4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	0
	91	105	106	120	121	135	136	150	151	165	166	180
STEAP-1	LREVIHPLATSEQQY	FYKIPILVINKVLP	VSITLLALVYLP	GVH	AAIVQLHNGTKYKKE	PHMLDKWMLTRKQFG	LLSFFFAVLAHAYSL					180
STEAP-2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	76
STEAP-3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	0
STEAP-4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	0
	181	195	196	210	211	225	226	240	241	255	256	270
STEAP-1	SYPMRRSRVYGLAN	AYQQVQCKEDANIE	HDVWRMEIYVSI	GIV	GLATLALLAVTSIPS	VSDSLTWREFRFTIQS	KLGLVSLLLGTHAL					270
STEAP-2	CLPMRRSERVLEAM	AYQQVHANIEANSWE	EEVWRMEIYVSI	FGIM	SLGLLSLLAVTSIPS	VSNALNWRREFSFQIS	TLGYVALLISTFHVTL					166
STEAP-3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	68
STEAP-4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	82
	271	285	286	300	301	315	316	330	331	345	346	360
STEAP-1	IPANWKWIDIKQFVW	YTPPTFENIAVFLPIV	VLIHFKSILFLPCLRK	KILKIRPHGHE	EDVTKI	NKTEICSQL						360
STEAP-2	YIGWKRA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	173 (SEQ ID NO:2)
STEAP-3	VYGGKRFLLSPSNLW	YLPAAKVLGLIIPCT	VLIHFKFVLHPCVDN	TLTRIRQGV	ERNSKH	-----						128 (SEQ ID NO:2)
STEAP-4	TYGWTRAFESPYKF	YLPPTFTXTLLVPCV	RSSWAKALFXLPCIQ	P	-----	-----						128 (Portion of SEQ ID NO:8)

FIG. 14A

26x



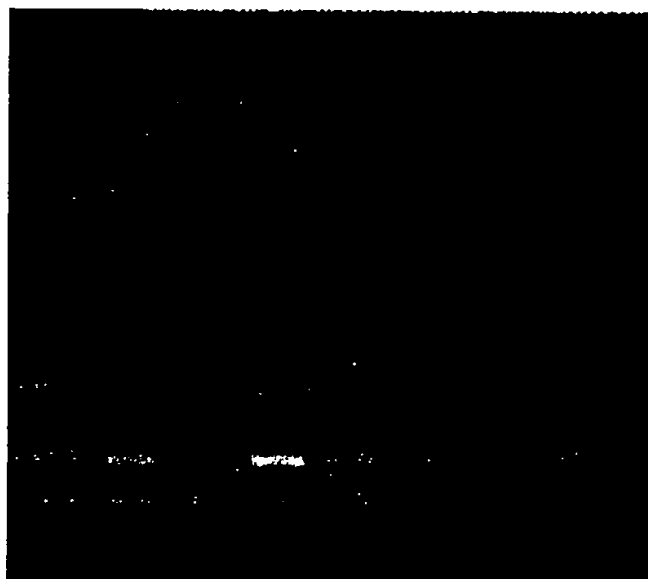
1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg control

FIG. 14B

1 2 3 4 5 6 7 8

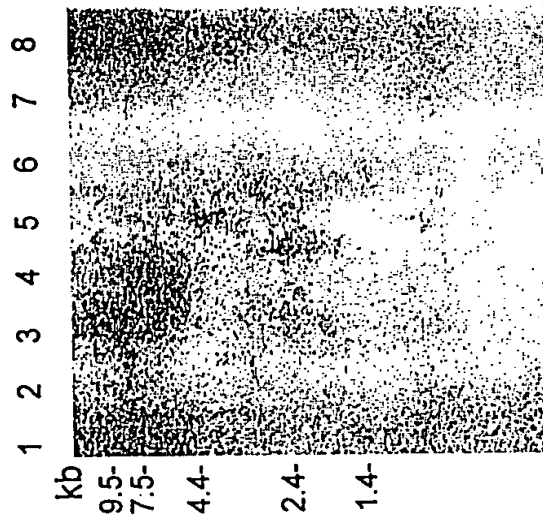
25x

30x



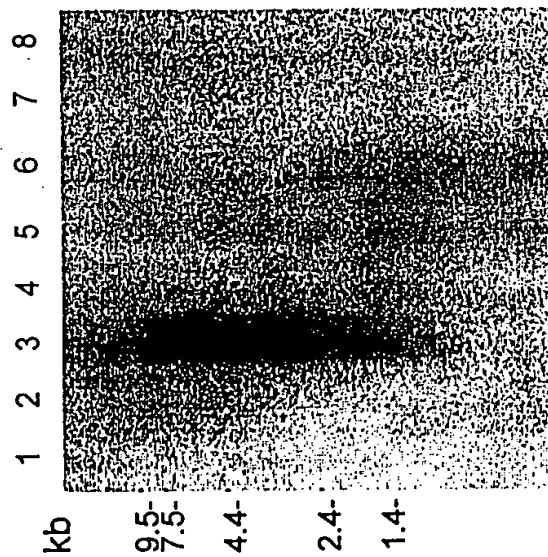
1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 15A



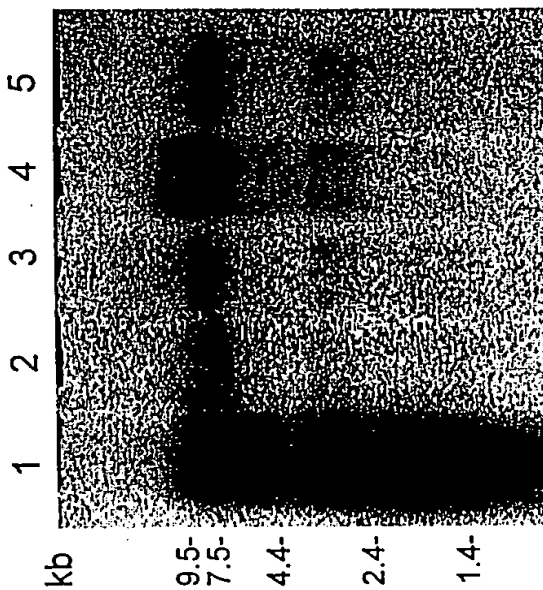
1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

FIG. 15B



1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

FIG. 15C



1. Prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI

FIG. 16

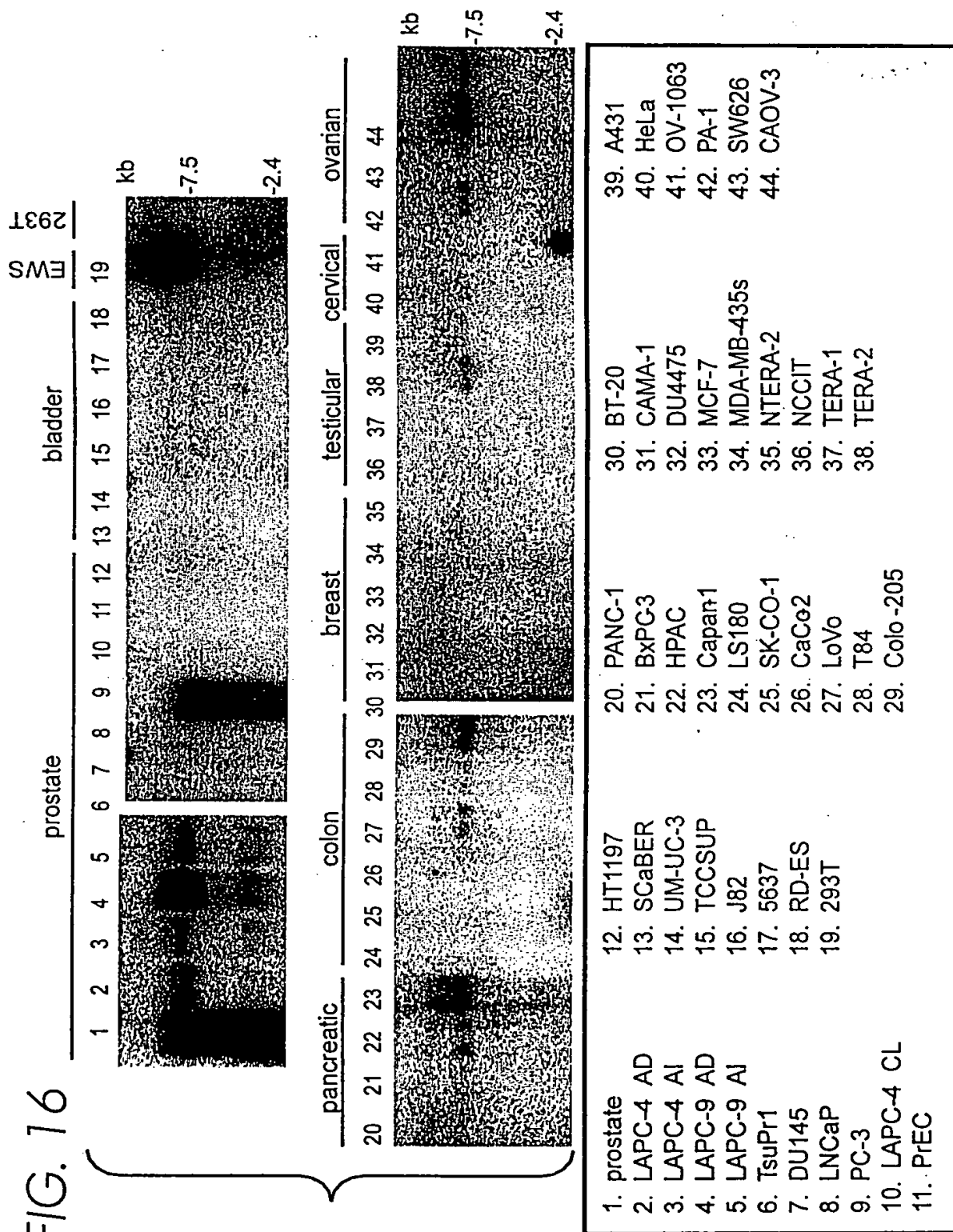


FIG. 17

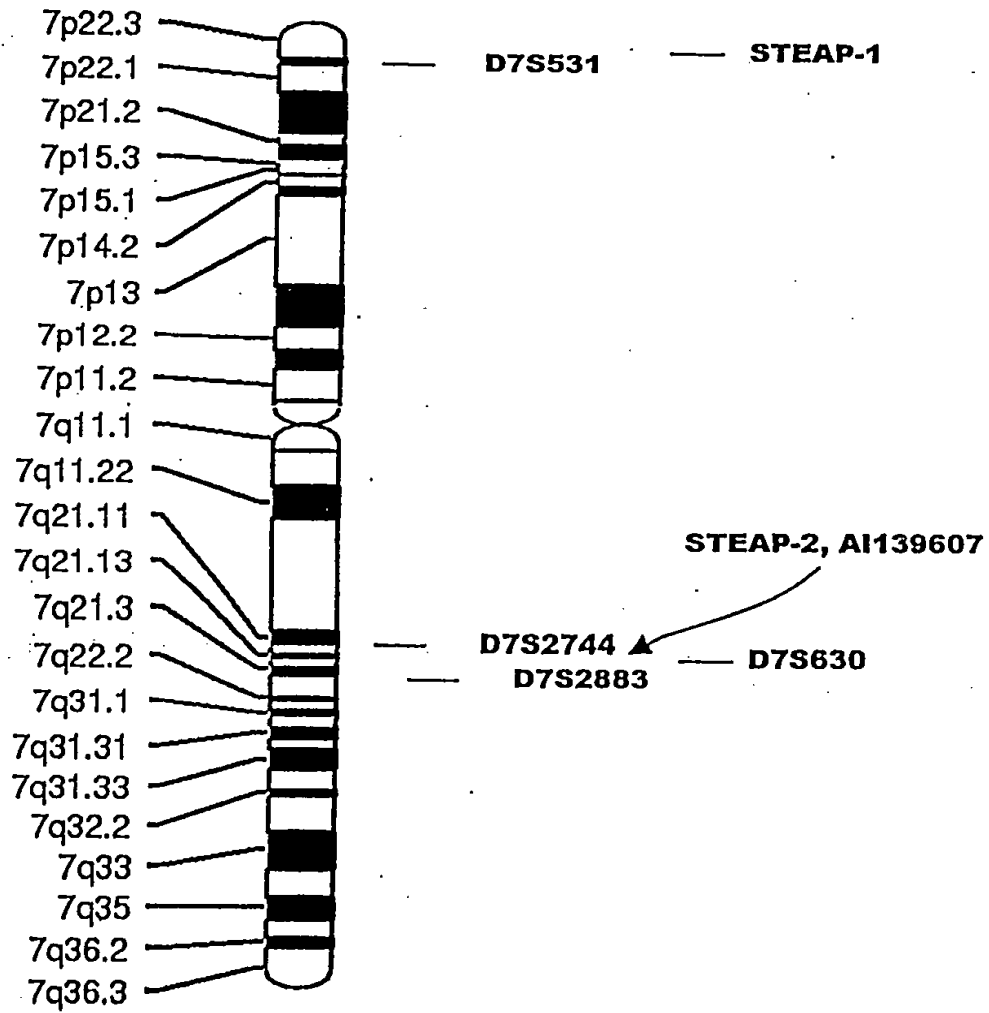


FIG. 19

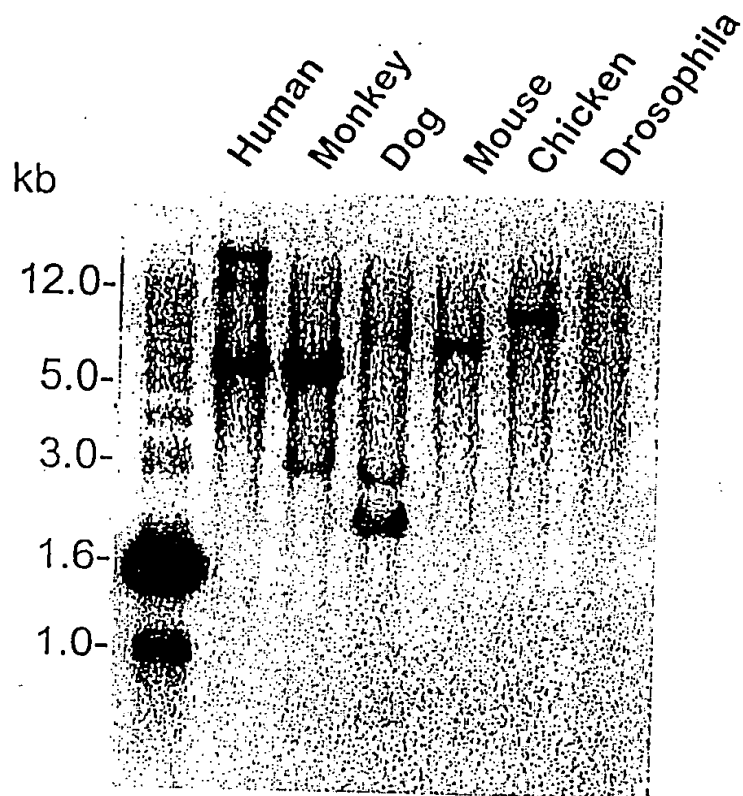
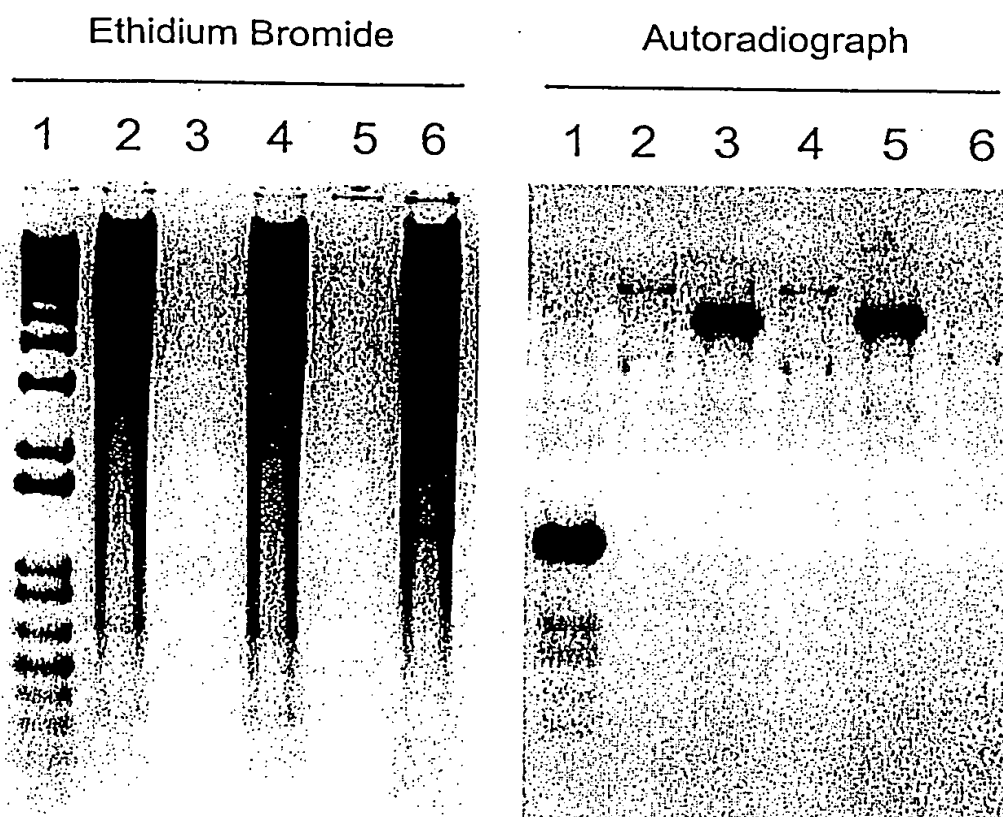


FIG. 20

**Lanes**

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3